## AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning at line 24 of page 27 as follows:

The analysis was carried out using robust multi-array analysis (RMA), since small data sets were analyzed. Software for RMA is available online ~~at the website www.bioconductor.org,~~ for use in the R 1.70 package for statistical computing ~~(www.r-project.org)~~.

Please amend the paragraph beginning at line 1 of page 28 as follows:

To determine candidate markers of rejection, three criteria were applied to the normalized data. First, data were filtered to include genes present above background on at least one array. Second, Significance Analysis of Microarrays (SAM~~; http://www-stat.stanford.edu/~tibs/SAM/~~) was used to correct for multiple comparisons and to select candidate markers of rejection using genes that were differentially expressed with an estimated overall false-discovery rate <0.10. Third, we required at least a 25% change in expression between Rejection and Control samples for a transcript to be of interest. The identities of differentially expressed genes were determined using annotation databases ~~(www.netaffx.com)~~ or via BLAST searches of the corresponding expressed sequence tags.

Please amend the paragraph beginning at line 13 of page 28 as follows:

To determine whether candidate markers of rejection responded to immunosuppressive therapy, expression data was analyzed for these transcripts in patient samples, which were isolated from patients who had rejected the cardiac allografts. These samples were assessed in order to determine whether the expression pattern of the candidate genes paralleled what was seen in the subjects at baseline. ~~**[is this correct?]**~~

Please amend the paragraph beginning at line 3 of page 29 as follows:

The capacity of candidate markers to distinguish Control, Rejection, and Post-Rejection samples was assessed using hierarchical clustering. Clusters were constructed using average linkage clustering and Pearson correlation coefficients as a measure of similarity using Cluster software and displayed using Treeview software ~~(http://rana.lbl.gov)~~.

Please amend Table 2 beginning at line 7 of page 33 as follows:

Table 2. Candidate Expression Markers of Cardiac Allograft Rejection

| **Gene (Gene Symbol)** | **Protein Type/ Cellular Pathway** | **Fold-Change (Rejection versus Control)** | **Fold-Change (Post-Rejection versus Control)** | **Probe-Set ID*** | **UniGene ID†** |
|---|---|---|---|---|---|
| ubiquinol-cytochrome c reductase binding protein (UQCRB) | Oxidative respiration | 2.25 | 1.3 | 205849_s_at | Hs.131255 |
| basic transcription factor 3 (BTF3) | RNA translation | 1.57 | 1.24 | 208517_x_at 211939_x_at | Hs.446567 |
| suppression of tumorigenicity 13 (ST13) | Tumor suppressor | 1.43 | 1.19 | 207040_s_at | Hs.377199 |
| cullin 4A (CUL4A) | Cell cycle/DNA replication | 1.34 | 1.1 | 201423_s_at | Hs.270788 |
| telomeric repeat binding factor 2, interacting protein (TERF2IP) | Transcription factor | 1.31 | 1.15 | 201174_s_at | Hs.274428 |
| arrestin, beta 2 (ARRB2) | Intracellular signaling | 0.75 | 0.79 | 203388_at | Hs.435811 |
| EST | | 0.75 | 0.99 | 207365_x_at | Hs.435123 |
| EST | | 0.74 | 0.96 | 207730_x_at | Hs.406701 |
| EST | | 0.74 | 0.86 | 205781_at | Hs.164410 |

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|---|---|---|---|---|---|
| aminopeptidase puromycin sensitive (NPEPPS) | Proteinase | 0.73 | 0.91 | 201454_s_at | Hs.293007 |
| phosphatidylinositol glycan, class B (PIGB) | Cell surface protein | 0.73 | 0.8 | 205452_at | Hs.259326 |
| adenomatosis polyposis coli (APC) | Tumor suppressor | 0.72 | 0.9 | 216933_x_at | Hs.75081 |
| B-cell CLL/lymphoma 7A (BCL7A) | Cell cycle/DNA replication | 0.72 | 0.98 | 210679_x_at | Hs.371758 |
| endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4 (EDG4) | Cell cycle/DNA replication | 0.72 | 0.81 | 206722_s_at 206723_s_at | Hs.122575 |
| interleukin 17 receptor (IL17R) | Interleukin receptor | 0.72 | 0.79 | 205707_at | Hs.129751 |
| placental growth factor (PGF) | Hormone/ Angiogenesis Factor | 0.72 | 0.96 | 215179_x_at | Hs.252820 |
| EST | | 0.7 | 0.85 | 220712_at | Hs.493129 |
| EST | | 0.7 | 0.9 | 215558_at | Hs.485406 |
| EST | | 0.7 | 0.9 | 220071_x_at | Hs.14347 |
| nuclear factor of activated T-cells 5, tonicity-responsive (NFAT5) | Transcription factor | 0.7 | 0.83 | 208003_s_at | Hs.86998 |
| EST | | 0.69 | 0.89 | 221205_at | |
| EST | | 0.69 | 0.89 | 215978_x_at | Hs.447720 |
| baculoviral IAP repeat-containing 1 (BIRC1) | Apoptosis | 0.68 | 0.76 | 204861_s_at | Hs.79019 |
| leukocyte immunoglobulin-like receptor, subfamily B, member 3 (LILRB3) | Leukocyte receptor | 0.68 | 0.81 | 210784_x_at 211135_x_at | Hs.306230 |
| EST | | 0.66 | 0.94 | 209703_x_at | Hs.288771 |
| transmembrane 6 superfamily member 2 (TM6SF2) | Cell surface protein | 0.66 | 0.88 | 210598_at | Hs.367829 |
| EST | | 0.65 | 0.9 | 215375_x_at | Hs.438377 |
| EST | | 0.65 | 0.94 | 215029_at | Hs.293563 |

| | | | | | |
|---|---|---|---|---|---|
| CASP8 and FADD-like apoptosis regulator (CFLAR) | Apoptosis | 0.59 | 0.73 | 211862_x_at<br>210564_x_at<br>208485_x_at<br>211317_s_at<br>214486_x_at | Hs.355724 |
| superoxide dismutase 2, mitochondrial (SOD2) | Oxidative stress | 0.56 | 0.83 | 221477_s_at | Hs.384944 |
| EST | | 0.55 | 0.84 | 216109_at | Hs.435249 |
| solute carrier family 16, member 3 (SLC16A3) | Membrane transport | 0.54 | 0.66 | 202856_s_at | Hs.386678 |
| stearoyl-CoA desaturase 4 (SCD4) | Fatty acid metabolism | 0.5 | 0.87 | 220232_at | Hs.379191 |

*Probe-Set ID: indicates the corresponding probe-set on the Affymetrix HU 133A microarray ~~– http://www.affymetrix~~.

†Unigene ID information are available online at NCBI website. ~~: http://www.ncbi.nlm.nih.gov/UniGene~~

EST indicates Expressed Sequence Tag